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ABSTRACT

Three examples of genetics and evolution simulation concerning Mendelian inheritance, genetic mapping, and natural selection are used to illustrate the use of simulations in modeling scientific/natural processes. First described is the HERED series, which illustrates such phenomena as incomplete dominance, multiple alleles, lethal alleles, linkage, sex-linkage, complementary genes, and epistasis, and simulates the hereditary mechanisms in particular species. A sample printout is used to explain the series. The second simulation discussed is LINKOVER, which involves genetic mapping and retains the essence of planning and performing crosses with living organisms while greatly speeding up the technique. The last simulation described is SELECT, a population genetics program based on simple colored bead models of natural selection in a one locus/two allele situation. It is concluded that, although some problems exist in using such computer simulations in genetics and evolution instruction, students' grasp of many difficult topics can be greatly enhanced through interaction with computer models. Twenty-five references are listed. (LMM)

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Computer Assisted Learning Research Group

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Genetics and Evolution

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May 1981

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GENETICS AND EVOLUTION

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INTRODUCTION

It is generally accepted that scientific subjects should not be taught without a strong practical component. However, practical work in genetics and evolution is severely constrained by several factors, the most obvious of which is time. This manifests itself in two ways. Firstly, experiments often have to be run for several or many generations for useful results to be obtained, and secondly, many species have relatively long generation times. Difficulties are encountered even with Drosophila and most species of educational interest are ruled completely out of the question. Also, experiments frequently involve quite large populations of organisms, the maintenance of which is a far from trivial task. Finally, although experience in the handling of experimental organisms is vitally important, mistakes made during the process of acquiring the necessary manipulative and observational skills frequently make the results of experiments unreliable or even meaningless in genetic terms.

The above are not arguments for omitting practical work with living organisms from courses on genetics and evolution, but arguments for supplementing it with other approaches. One such alternative approach is to encourage students to interact with models of the genetic or evolutionary systems under consideration, altering parameters systematically and observing and interpreting outcomes. Genetic systems are often particularly amenable to modelling, certainly

compared to many ecological or physiological systems, because they are quite well defined and because they can be simplified to increase their educational impact.

Physical models, the best known of which involve using coloured beads to represent populations of different alleles, have long been used in the teaching of genetics (Sheppard [illegible]4; Heath 1975). The great benefit in handling beads is that students become thoroughly familiar with the mechanism and underlying assumptions of the models. However, the generation of data in such investigations is a very slow and rather tedious process, effectively ruling out even moderately large populations or more than a very few generations.

These problems can be overcome by taking advantage of the fantastic speed, accuracy and stamina of modern electronic computers. Most students find using computer simulations highly motivating and that their grasp of difficult genetic concepts is enhanced. However, there is a danger that computer output is accepted uncritically. This becomes less likely when the use of such simulations is integrated with laboratory work using living organisms, interpretation of secondhand data and the use of bead (or similar) models. Such a practical "package" can be extremely effective educationally (Garbutt et al 1979).

There would be no point in introducing computer simulations into a genetics or evolution course if the teacher was not convinved that the students' understanding of these subjects would be improved as a result. Whether such improvement is likely in any particular instance can be judged only by the teacher running the programs himself. Descriptions and static diagrams cannot adequately represent dynamic interaction with computer simulations. Nevertheless, three examples of simulations in

the field of genetics and evolution (concerning Mendelian inheritance, genetic mapping and natural selection) are discussed below.

MENDELIAN GENETICS

Probably the earliest teaching simulations in genetics concerned the generation of statistically 3:1, 1:2:1, 9:3:3:1, etc ratios. However, some of the best programs simulating Mendelian genetics, the HERED series written for the Schools Council Computers in the Curriculum Project (Leveridge 1978), go far beyond mono- and di-hybrid ratios, while remaining firmly rooted in the elementary principles and in practical work with living organisms. Among the phenomena illustrated by the programs are incomplete dominance, multiple alleles, lethal alleles, linkage, sex-linkage, complementary genes and epistasis.

Four of the five programs in the series simulate the heriditary mechanisms in particular species:

HERED1	Drosophila melanogaster (fruitfly)
HERED2	Mus musculus (house mouse)
HERED3	Homo sapiens (man)
HERED4	Lycopersicum esculentum (tomato)

HERED5 is rather different in that it simulates multifactorial inheritance in a hypothetical organism and will not be further considered here.

A sample printout from each of the programs will be used to illustrate the series. The original programs were written before microcomputers and modern computer terminals were available and the assumption had to be made that lower-case letters would not necessarily be available on the user's machine. Consequently, upper-case letters for gene symbols, etc in the sample printouts should not be taken to imply genetic

dominance.

HERED1

In response to the question 'HOW MANY GENES?' the user typed '1' (Figure 1). This causes the program to simulate monohybrid inheritance in Drosophila melanogaster. The next question asked was 'WHAT IS ITS SYMBOL?' and the response was 'VG'. The gene will therefore be that which gives rise to vestigial or wild-type wings. The conventional notation for the two relevant alleles is vg and +. The user then had to specify the characters of the male and female parents. When a parent is specified de nova it is always homozygous for the gene(s) in question. So, when the user typed 'VG' for the male that parent had vestigial wings and the genotype vgvg. Similarly, when '+' was typed for the female that parent had wild-type wings and the genotype ++. The original parents are given the code numbers 1 and 2 so that they can be used in further crosses if desired. To effect the cross:

(1)		(2)
♂		♀
vgvg	x	++

the user asked for a family of 20 offspring to be generated.

FIGURE 1 here

The code numbers (3 - 22), sex and phenotypes of these 20 offspring are printed. All are wild-type indicating that the vestigial character is genetically recessive to the wild-type. There is an excess of females in this family, but the excess is not statistically significant.

The user typed 'YES' to the question 'ANOTHER CROSS?' and so was invited to state which organisms are to be the parents of the next generation. The male whose code number is 21 and the female whose code number is 23 were chosen. Female number 23 is from outside the family and so has to be specified genetically. The user has stated that it shall be homozygous vestigial (or recessive) in character and so the next cross is:

(21) (23)

♂ ♀

vg+ x vgvg

This is effectively a backcross of an F_1 organism with its recessive parental type, so a 1:1 ratio is to be expected in the next generation with respect to both vestigial:wild-type and male:female. There are no statistically significant deviations from expectation.

The other characters which can be studied (singly or in combination) using HERED1 are black body (+/b), ebony body (+/e), curled wing (+/cu), brown eye (+/bw), scarlet eye (+/st) and white eye (+/w).

HERED2

The user has specified that the program is to simulate the monohybrid inheritance of albinoism in the house mouse (Figure 2). Mouse number 1 is the male parent and is genotypically ++. Consequently he has wild-type agouti fur (in which each hair has a black base and yellow tip) and black eyes. The female parent (number 2) is genotypically cc and is albino, having white fur and red eyes.

FIGURE 2 here

All 20 of the offspring have agouti fur and black eyes, demonstrating that the albino character is recessive to wild-type. There are approximately equal numbers of male and female mice in the family.

The user then decided to order a sib-mating between mouse number 4 and mouse number 6. Since both mice must be heterozygotes a 3:1 ratio in favour of wild-type is to be expected in the F_2 generation. The observed deviation from expectation is not statistically significant and neither is there a significant excess of one sex over the other.

HERED2 concentrates on the genes affecting colour of the fur and eyes. However, it also simulates pituitary dwarfism (+/dw), dwdw mice being sterile. The allele for yellow fur (A^y) is lethal in the homozygous state, resulting in 1:2 ratios where 1:2:1 ratios might be expected.

HERED3

The user has specified a cross between a man homozygous for the allele for tongue rolling and a woman homozygous for the allele for inability to roll the tongue (i.e. tongue flat). All eight of their children are tongue rollers, so clearly this character is dominant. Incidently, the statistically significant bias towards females in this family serves only to emphasise the stochastic nature of this program (and indeed many others in genetics and evolution).

FIGURE 3 here

The user went on to order a cross between one of the sons (number 6), who must be heterozygous (Tt), and a female from another family (number 11), who is homozygous for inability to tongue roll (tt). The resulting family of sixteen children does not show a significant

deviation from the expected 1:1 ratio with respect to either tongue rolling or gender.

The other genes which can be investigated using HERED3 are those controlling the ABO blood group, the Rhesus blood group and red-green colour blindness.

HERED4

The user has specified a monohybrid cross between a tomato plant homozygous for hairless hypocotyl (called stem here for conciseness) (h1h1) and a wild-type or hairy stemmed plant (++). The former is the pollen (or male) parent and the latter is the ovule (or female) parent. The hairy condition is clearly dominant as can be seen in the F_1 family. One plant (number 3) is specified as both the pollen and the ovule parent of the next generation. In other words, it is selfed. The 13:7 ratio in F_2 is not significantly different from the 3:1 ratio expected.

FIGURE 4 here

The other genes available in HERED4 are those for green hypocotyl (+/bls), green cotyledon (+/xa-3), solanifolia (+/sf) and potato leaf (+/c).

GENETIC MAPPING

Genetic mapping in the teaching laboratory, using the 3-point test-cross technique with Drosophila, is perfectly possible, but quite time-consuming. The simulation LINKOVER (in which the actual program is named LNKOVR), published as part of the Chelsea Science Simulation Project (Murphy 1975), was designed to retain the essence of planning and performing crosses with living organisms while greatly speeding up the process. As well as

permitting students to build up their own genetic map of an "electronic organism", it reinforces the concepts of linkage and crossing-over.

As in the HERED programs, the genes, although printed as upper-case letters, should be read as lower-case, and hence recessive mutants. The corresponding wild-type dominant alleles are +. The ten genes (a, c, h, j, k, m, p, r, t and y) are scattered within a single linkage group and the user's objective is to map them as accurately as possible.

FIGURE 5 here

Without knowing the true order of the genes the user has specified that he is interested in crosses involving the genes j, r and t (Figure 5). Effectively, a strain of this hypothetical organism which is homozygous recessive at these three loci and another which is homozygous at the loci has been brought into existence. The two strains are then crossed to produce an F_1 heterozygote:

$$\frac{j\ r\ t}{j\ r\ t} \times \frac{+\ +\ +}{+\ +\ +} \rightarrow \frac{j\ r\ t}{+\ +\ +}$$

The F_1 hybrid is then back- or test-crossed with the homozygous recessive strain:

$$\frac{j\ r\ t}{+\ +\ +} \times \frac{j\ r\ t}{j\ r\ t}$$

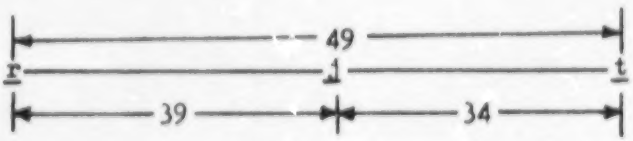
resulting in another generation in which may be found up to eight phenotypic classes caused by crossing-over during meiosis in the F_1 organisms (crossing-over in the homozygous recessive strain being

undetectable owing to its homozygosity).

First, it is necessary to determine the order of the genes within the linkage group. The rarest pair of phenotypic classes correspond to the double cross-over and in this case the pair is +rt/j++. In the double cross-over the middle gene is isolated from its partners, so j must be in the middle and the order must be:

r——j——t

In a family of 100 organisms the genes r and j have become separated a total of (8+5+11+15) or 39 times. This is equivalent to 39 percent and indicates that the genes r and j are 39 map units apart. Similarly, the genes j and t have become separated a total of (8+5+8+13) or 34 times. Thus the genes j and t are 34 map units apart. Finally, the genes r and t have become separated a total of (8+13+11+15) or 49 times. Thus the genes r and t are 49 map units apart. This data can be represented diagrammatically:

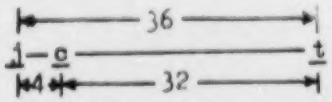


This dramatically illustrates the underestimation of separation with increased distance between genes.

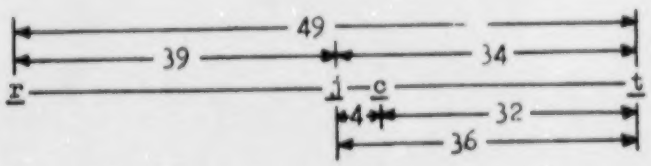
Having established part of the genetic map the user then opts to do a cross involving the genes j and t as before and the new gene o. It can be seen that there appear to be only six phenotypic classes, not eight. The rarest pair of classes (each with a frequency of zero) are the missing two, which are +jt/o++. The middle gene must be o and the order is:

j——c——t

Again in a family of 100 organisms the genes j and c have become separated (0+0+3+1) or 4 times. They are thus 4 map units apart. Similarly, c and t are 32 map units apart and j and t are 36 map units apart. Representing the data diagrammatically:



The two partial maps can now be put together:



And so the user can proceed until all the genes have been at least ordered. Crosses involving genes known to be adjacent allow the map to be drawn up with maximum precision. It is educationally effective, and also enjoyable for all concerned, to set different groups of students competing against each other in a race for "the map". This encourages groups to think out optimal crossing strategies, rather than adopt a "hit and miss" approach (Dean and Murphy 1973).

FIGURE 6 here

Once the genetic map has been completed it is possible to do something which would be quite impossible if the experiment had been performed with real organisms — that is, to compare the genetic and the "cytological" maps. The "cytological" map (Figure 6) can be supplied to the students and they can redraw it to the same scale as their genetic map (Figure 7). The phenomena of end- and centromere-interference are apparent from this comparison and can lead to some useful discussion.

FIGURE 7 here

It is possible for the teacher to change the genes, their number and/or their locations to suit the needs of particular classes. It is also possible to set up the genes in "repulsion" rather than the much easier "coupling" which has been assumed so far.

POPULATION GENETICS

SELECT is a program produced by the Computers in the Undergraduate Science Curriculum Project (Lal et al 1978; Wood 1979; Garbutt et al 1979) and is an enhancement of the program EVOLUT published as part of the Chelsea Science Simulation Project (McCormick 1975). Both programs are based on simple coloured bead models of natural selection in a one locus/two allele situation, and this is reflected in the dialogue between the user and the computer.

The idea is that a pool of gametes is created, twice the size of the population of organisms being considered. There are two types of gamete, corresponding to the two alleles present in the population, and the proportions of the two alleles in the pool is the same as that in the parental population at the time of reproduction. Pairs of gametes are drawn randomly from the pool to form zygotes. Each zygote (which has to have one of the three possible genotypes) is allowed to survive or not according to the relative fitness of its genotype. Thus, if the relative fitness of a particular genotype was 0.25, then zygotes of that genotype will be permitted to survive, and contribute reproductively to the next generation, an average of 25 percent of the occasions when drawn from the pool. If a zygote survives this selection then it is recorded as being present in the next generation, if it fails to survive it is not

so recorded. The beads are then returned to the pool and the whole process repeated. With a population size of 100, there would be 200 beads in the pool and pairs would be withdrawn and returned 100 times. At this stage, by noting the numbers of each of the three genotypes recorded, it would be possible to see what effect one generation of selection had on the gene pool. A new gamete pool is then made up with the alleles in the same proportions as in the recorded generation and the cycle begun again.

It can easily be appreciated how tedious this iterative process is when performed by hand. SELECT (Figure 8) allows the above operations (and more) to be performed very much more quickly, enabling quite sophisticated investigations to be carried out by students. In the printout the two alternative alleles are designated Y and R (corresponding to yellow and red beads).

FIGURE 8 here

The user has decided initially to have a population of 200 organisms. Each generation will produce sufficient zygotes to keep the population at this size, but the population size will decline if not all survive to reproductive age. The effect population size has then been halved, because the user has opted to have only 50 percent of the adults actually involved in reproduction. The whole of the population is inbreeding, although any proportion could have been specified between 0 and 100 percent. The program requires the user to state the initial distribution (as percentages) of the three genotypes in the population and he has opted for 25 YY : 50 YR : 25 RR. The population thus starts off in Hardy-Weinberg equilibrium (assuming no inbreeding or differential survival prior to Generation 0), but, where it applies, Hardy-Weinberg equilibrium would be acheived after only one generation anyway. Finally,

the user has to specify the relative fitness of each of the three genotypes and has decided that the heterozygote shall have a relative fitness of 1 and the two homozygotes each a relative fitness of 0.3. Heterozygote advantage, in an inbreeding situation, is therefore being modelled.

In Generation 0 the initial distribution of the three genotypes can be seen. There are 50 YY, 100 YR and 50 RR individuals, giving a total of 200. Inbreeding has approximately halved the number of heterozygotes by Generation 1, but the lower fitness of the homozygotes means that they too are approximately half the expected number. The number of heterozygotes has not continued to fall by half in each generation, as would be expected with 100 percent inbreeding in the absense of selection, but remains fluctuating about to 50 level. The numbers of each of the two homozygotes also fluctuate, but by Generation 10 genetic drift has resulted in there being about twice the number of YY as RR individuals.

SELECT can be used to enable small groups of students to investigate issues within the field of population genetics and evolution. By altering the population size genetic drift can be explored, as it can by altering the percentage of the population breeding. However, the latter parameter also permits the founder principle to be studied. The impact of inbreeding can be investigated by systematically altering the percentage of inbreeding. The significance of the Hardy-Weinberg equilibrium becomes quite apparent by noting the change in the numbers of each genotype from the initial generation to Generation 1, and then the change from Generation 1 to 2, etc. Many different models of natural selection can be set up by choosing appropriate values for the different relative fitnesses. For instance, YY = 1, YR = 1 and RR = 0 represents homozygote lethality and YY = 0.5, YR = 1 and RR = 0

represents something akin to sickle cell anaemia in the presence of malaria. Finally, there are the almost limitless interactions between these parameters. The sample printout shows an attempt to balance the effect of inbreeding by applying heterozygote advantage. Because of the relatively small effective population size the effect of drift is apparent, but it is clear that balance has almost been attained.

CONCLUSIONS

There are numerous benefits, and a few problems, in using computer simulations in the teaching of genetics and evolution (Carbutt et al 1979). However, there can be no doubt that the students' grasp of many difficult topics can be enhanced greatly through interaction with computer models.

The examples outlined in this chapter were selected from quite a wide range of published material (for example Appleton 1973; Crosby 1973; Schaffer and Mettler 1974; Vincent 1975; Skibinski 1977; Hull 1977, 1978; North and Dent 1978; Smythe and Lovatt 1979). Good programs have been written for machines ranging from programmable calculators (Beare 1978; Hewitson 1978a,b,c,d,e) to massive mainframe computers in the case of PLATO (Hyatt et al 1972). It is anticipated that many more worthwhile programs will be written as microcomputers give practising teachers unparalled opportunities to develop their own ideas. Such teachers are urged to maintain the tradition of high standards in programming and educational documentation and to make their work available to a much wider audience than just their own students.

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LEGENDS AND SOURCES FOR FIGURES

FIGURE 1 Sample printout from the program HERED1. Characters typed by the user have been underlined, the rest were printed by the computer.

(Source: LEVERIDGE 1978)

FIGURE 2 Sample printout from the program HERED2. Characters typed by the user have been underlined, the rest were printed by the computer.

(Source: LEVERIDGE 1978)

FIGURE 3 Sample printout from the program HERED3. Characters typed by the user have been underlined, the rest were printed by the computer.

(Source: LEVERIDGE 1978)

FIGURE 4 Sample printout from the program HERED4. Characters typed by the user have been underlined, the rest were printed by the computer.

(Source: LEVERIDGE 1978)

FIGURE 5 Sample printout from the program LNKOVR. Characters typed by the user have been underlined, the rest were printed by the computer.

(Source: MURPHY 1975)

FIGURE 6 The "cytological" map from the program LNKOVR.

(Source: MURPHY 1975)

FIGURE 7 Comparison of the "cytological" and genetic maps from the program LNKOVR.

(Source: MURPHY 1975)

FIGURE 8 Sample printout from the program SELECT. Characters typed by the user are underlined, the rest were printed by the computer.

(Source: GARBUTT et al 1979)

FIGURE 1

INHERITANCE IN DROSOPHILA MELANOGASTER

HOW MANY GENES ? 1

WHAT IS ITS SYMBOL ? VG

PARENTS
MALE CHARACTERS
? VG
FEMALE CHARACTERS
? +

HOW MANY OFFSPRING ? 20

OFFSPRING

NO.	SEX	WINGS	NO.	SEX	WINGS
3	M	WILD	4	M	WILD
5	F	WILD	6	M	WILD
7	F	WILD	8	M	WIL
9	M	WILD	10	F	WILD
11	F	WILD	12	F	WILD
13	F	WILD	14	F	WILD
15	F	WILD	16	F	WILD
17	F	WILD	18	M	WILD
19	F	WILD	20	F	WILD
21	M	WILD	22	F	WILD

ANOTHER CROSS ? YES

MALE PARENT ? 21
FEMALE PARENT ? 23
CHARACTERS
? VG

HOW MANY OFFSPRING ? 20

OFFSPRING

NO.	SEX	WINGS	NO.	SEX	WINGS
24	M	WILD	25	M	SMALL
26	M	SMALL	27	F	WILD
28	M	WILD	29	M	WILD
30	F	SMALL	31	M	SMALL
32	M	SMALL	33	M	WILD
34	F	SMALL	35	F	SMALL
36	M	SMALL	37	M	SMALL
38	M	WILD	39	F	SMALL
40	F	WILD	41	F	SMALL
42	M	WILD	43	M	WILD

ANOTHER CROSS ? NO
DO YOU WISH TO START AGAIN ? NO

FIGURE 2

INHERITANCE IN MICE

```
HOW MANY GENES ? 1

WHAT IS ITS SYMBOL ? C

PARENTS
  MALE CHARACTERS
 ? 4
  FEMALE CHARACTERS
 ? C

HOW MANY OFFSPRING  ? 20

OFFSPRING

 NO.  SEX   FUR     EYES        NO.  SEX   FUR     EYES

  3    F    AGOUTI  BLACK       4    M    AGOUTI  BLACK
  5    M    AGOUTI  BLACK       6         AGOUTI  BLACK
  7    M    AGOUTI  BLACK       8    F    AGOUTI  BLACK
  9    F    AGOUTI  BLACK       10   F    AGOUTI  BLACK
  11   M    AGOUTI  BLACK       12   M    AGOUTI  BLACK
  13   M    AGOUTI  BLACK       14   M    AGOUTI  BLACK
  15   M    AGOUTI  BLACK       16   F    AGOUTI  BLACK
  17   M    AGOUTI  BLACK       18   F    AGOUTI  BLACK
  19   F    AGOUTI  BLACK       20   M    AGOUTI  BLACK
  21   M    AGOUTI  BLACK       22   F    AGOUTI  BLACK

ANOTHER CROSS ? YES

MALE PARENT  ? 4
FEMALE PARENT ? 6

HOW MANY OFFSPRING  ? 20

OFFSPRING

 NO.  SEX   FUR     EYES        NO.  SEX   FUR     EYES

  23   M    AGOUTI  BLACK       24   M    WHITE   RED
  25   M    WHITE   RED         26   F    WHITE   RED
  27   M    AGOUTI  BLACK       28   F    WHITE   RED
  29   F    AGOUTI  BLACK       30   M    AGOUTI  BLACK
  31   F    AGOUTI  BLACK       32   M    AGOUTI  BLACK
  33   M    AGOUTI  BLACK       34   M    AGOUTI  BLACK
  35   F    WHITE   RED         36   M    WHITE   RED
  37   M    AGOUTI  BLACK       38   F    AGOUTI  BLACK
  39   F    AGOUTI  BLACK       40   F    AGOUTI  BLACK
  41   M    AGOUTI  BLACK       42   M    AGOUTI  BLACK

ANOTHER CROSS ? NO
DO YOU WISH TO START AGAIN ? NO
```

FIGURE 3

HUMAN INHERITANCE

HOW MANY GENES ? 1

WHAT IS ITS SYMBOL ? T

PARENTS
MALE CHARACTERS
? TR
FEMALE CHARACTERS
? TF

HOW MANY CHILDREN, ? 8

CHILDREN

NO.	SEX	TONGUE	NO.	SEX	TONGUE
3	F	ROLL	4	F	ROLL
5	F	ROLL	6	M	ROLL
7	F	ROLL	8	F	ROLL
9	F	ROLL	10	F	ROLL

ANOTHER FAMILY ? YES

MALE PARENT ? 6
FEMALE PARENT ? 11
CHARACTERS
? TF

HOW MANY CHILDREN ? 16

CHILDREN

NO.	SEX	TONGUE	NO.	SEX	TONGUE
12	M	FLAT	13	F	FLAT
14	M	ROLL	15	M	FLAT
16	M	FLAT	17	F	ROLL
18	M	FLAT	19	M	FLAT
20	F	FLAT	21	F	FLAT
22	F	ROLL	23	F	ROLL
24	M	FLAT	25	M	FLAT
26	M	ROLL	27	F	FLAT

ANOTHER FAMILY ? NO
DO YOU WISH TO START AGAIN ? NO

FIGURE 4

INHERITANCE IN TOMATO PLANTS

HOW MANY GENES ? 1

WHAT IS ITS SYMBOL ? HL

PARENTS
POLLEN PLANT CHARACTERS
? HL
OVULE PLANT CHARACTERS
? 4

HOW MANY OFFSPRING ? 12

OFFSPRING

NO.	STEM HAIRS	NO.	STEM HAIRS
3	HAIRY	4	HAIRY
5	HAIRY	6	HAIRY
7	HAIRY	8	HAIRY
9	HAIRY	10	HAIRY
11	HAIRY	12	HAIRY
13	HAIRY	14	HAIRY

ANOTHER CROSS ? YES

POLLEN PLANT ? 3
OVULE PLANT ? 3

HOW MANY OFFSPRING ? 20

OFFSPRING

NO.	STEM HAIRS	NO.	STEM HAIRS
15	HAIRY	16	HAIRY
17	HRLESS	18	HAIRY
19	HAIRY	20	HRLESS
21	HAIRY	22	HRLESS
23	HAIRY	24	HAIRY
25	HRLESS	26	HAIRY
27	HAIRY	28	HRLESS
29	HAIRY	30	HRLESS
31	HAIRY	32	HRLESS
33	HAIRY	34	HAIRY

ANOTHER CROSS ? NO
DO YOU WISH TO START AGAIN ? NO

FIGURE 5

```
THE LINKED GENES ARE A C H J K M P R T Y

GENE  1  ? J
GENE  2  ? R
GENE  3  ? T

TESTCROSS
---------

JRT        JRT
---   X    ---
+++        JRT

OFFSPRING PHENOTYPES
--------------------

JRT       22

+++       18

+RT        8

J++        5

++T        8

JR+       13

+R+       11

J+T       15

-------------

ANOTHER RUN ? YES


THE LINKED GENES ARE A C H J K M P R T Y

GENE  1  ? C
GENE  2  ? J
GENE  3  ? T

TESTCROSS
---------

CJT        CJT
---   X    ---
+++        CJT

OFFSPRING PHENOTYPES
--------------------

CJT       33

+++       31

++T        3

CJ+        1

+J+       19

C+T       13

-------------

ANOTHER RUN ? NO

END OF PROGRAM
```

FIGURE 6

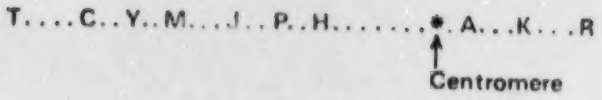

FIGURE 7

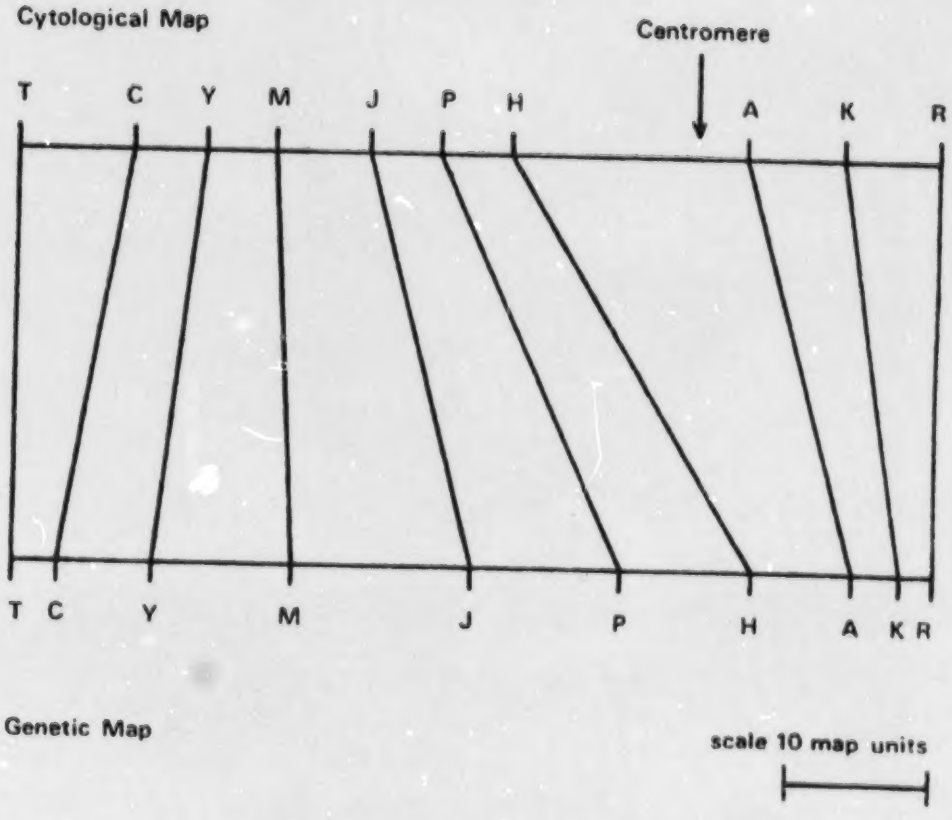

FIGURE 8

```
MAXIMUM POPULATION SIZE (50-500)  ?200

WHAT % OF POPULATION IS BREEDING (0-100)  ?50

WHAT % OF POPULATION IS INBREEDING (0-100)  ?100

WHAT IS INITIAL % OF EACH GENOTYPE (0-100,TOTAL = 100):-
   YY  ?25
   YR  ?50
   RR  ?25

WHAT IS RELATIVE FITNESS OF EACH GENOTYPE (0-1):-
   YY  ?.3
   YR  ?1
   RR  ?.3
```

GENERATION	YY	YR	RR	TOTAL
0	50	100	50	200
1	23	52	19	94
2	19	71	14	104
3	17	81	13	111
4	20	74	20	114
5	20	56	29	105
6	23	49	26	98
7	14	49	20	83
8	22	55	19	96
9	25	57	15	97
10	31	52	16	99

```
MORE  ?NO
```

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COMPUTER-ASSISTED LEARNING RESEARCH GROUP

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Ann Jones, Institute of Educational Technology, The Open University, Walton Hall, MILTON KEYNES, MK7 6AA, England.

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38	I. Every, and E. Scanlon; (1983) An Evaluation of the CAL at the Summer School for the Course S271 - Discovering Physics.
39	E. Scanlon, C. Hawkridge, R. Evertz; (1983) Modelling Physics Problem Solving: Production Rule Models of Two Problems.